

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: De Robertis, Edward M.
Bouwmeester, Tewis
- (ii) TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing Factors
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Majestic, Parsons, Siebert & Hsue
(B) STREET: Four Embarcadero Center, Suite 1100
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 94111-4106
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/878,474
(B) FILING DATE: 18-JUN-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/020,150
(B) FILING DATE: 20-JUN-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Siebert, J. Suzanne
(B) REGISTRATION NUMBER: 28,758
(C) REFERENCE/DOCKET NUMBER: 3100.002US1
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415/248-5500
(B) TELEFAX: 415/362-5418

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Leu Leu Asn Val Leu Arg Ile Cys Ile Ile Val Cys Leu Val Asn
1 5 10 15
Asp Gly Ala Gly Lys His Ser Glu Gly Arg Glu Arg Thr Lys Thr Tyr
20 25 30
Ser Leu Asn Ser Arg Gly Tyr Phe Arg Lys Glu Arg Gly Ala Arg Arg
35 40 45
Ser Lys Ile Leu Leu Val Asn Thr Lys Gly Leu Asp Glu Pro His Ile
50 55 60
Gly His Gly Asp Phe Gly Leu Val Ala Glu Leu Phe Asp Ser Thr Arg
65 70 75 80
Thr His Thr Asn Arg Lys Glu Pro Asp Met Asn Lys Val Lys Leu Phe
85 90 95
Ser Thr Val Ala His Gly Asn Lys Ser Ala Arg Arg Lys Ala Tyr Asn
100 105 110
Gly Ser Arg Arg Asn Ile Phe Ser Arg Arg Ser Phe Asp Lys Arg Asn
115 120 125
Thr Glu Val Thr Glu Lys Pro Gly Ala Lys Met Phe Trp Asn Asn Phe
130 135 140
Leu Val Lys Met Asn Gly Ala Pro Gln Asn Thr Ser His Gly Ser Lys
145 150 155 160
Ala Gln Glu Ile Met Lys Glu Ala Cys Lys Thr Leu Pro Phe Thr Gln
165 170 175
Asn Ile Val His Glu Asn Cys Asp Arg Met Val Ile Gln Asn Asn Leu
180 185 190
Cys Phe Gly Lys Cys Ile Ser Leu His Val Pro Asn Gln Gln Asp Arg
195 200 205
Arg Asn Thr Cys Ser His Cys Leu Pro Ser Lys Phe Thr Leu Asn His
210 215 220

Leu	Thr	Leu	Asn	Cys	Thr	Gly	Ser	Lys	Asn	Val	Val	Lys	Val	Val	Met
225					230					235					240
Met	Val	Glu	Glu	Cys	Thr	Cys	Glu	Ala	His	Lys	Ser	Asn	Phe	His	Gln
				245					250					255	
Thr	Ala	Gln	Phe	Asn	Met	Asp	Thr	Ser	Thr	Thr	Leu	His	His		
		260						265					270		

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCCTAA AAGCGGCACA GTGCAGGAAC AGCAAGTCGC TCAGAAACAC TGCAGGGTCT	60
AGATATCATA CAATGTTACT AAATGTACTC AGGATCTGTA TTATCGTCTG CCTTGTGAAT	120
GATGGAGCAG GAAAACACTC AGAAGGACGA GAAAGGACAA AAACATATTC ACTTAACAGC	180
AGAGGTTACT TCAGAAAAGA AAGAGGAGCA CGTAGGAGCA AGATTCTGCT GGTGAATACT	240
AAAGGTCTTG ATGAACCCCA CATTGGGCAT GGTGATTTTG GCTTAGTAGC TGAAC TATTT	300
GATTCCACCA GAACACATAC AAACAGAAAA GAGCCAGACA TGAACAAAGT CAAGCTTTTC	360
TCAACAGTTG CCCATGGAAA CAAAAGTGCA AGAAGAAAAG CTTACAATGG TTCTAGAAGG	420
AATATTTTTT CTCGCCGTTT TTTTGATAAA AGAAATACAG AGGTTACTGA AAAGCCTGGT	480
GCCAAGATGT TCTGGAACAA TTTTTTGTTT AAAATGAATG GAGCCCCACA GAATACAAGC	540
CATGGCAGTA AAGCACAGGA AATAATGAAA GAAGCTTGCA AAACCTTGCC CTTCACTCAG	600
AATATTGTAC ATGAAACTG TGACAGGATG GTGATACAGA ACAATCTGTG CTTTGGTAAA	660
TGCATCTCTC TCCATGTTCC AAATCAGCAA GATCGACGAA ATACTTGTTT CCATTGCTTG	720
CCGTCCAAAT TTACCCTGAA CCACCTGACG CTGAATTGTA CTGGATCTAA GAATGTAGTA	780
AAGGTTGTCA TGATGGTAGA GGAATGCACG TGTGAAGCTC ATAAGAGCAA CTTCCACCAA	840

ACTGCACAGT TTAACATGGA TACATCTACT ACCCTGCACC ATTAAAAGGA CTGTCTGCCA 900
TACAGTATGG AAATGCCCAT TTGTTGGAAT ATTCGTTACA TGCTATGTAT CTAAAGCATT 960
ATGTTGCCTT CTGTTTCATA TAACCACATG GAATAAGGAT TGTATGAATT ATAATTAACA 1020
AATGGCATT TGTGTAACAT GCAAGATCTC TGTTCCATCA GTTGCAAGAT AAAAGGCAAT 1080
ATTTGTTTGA CTTTTTCTA CAAAATGAAT ACCCAAATAT ATGATAAGAT AATGGGGTCA 1140
AAACTGTTAA GGGGTAATGT AATAATAGGG ACTAACAACC AATCAGCAGG TATGATTTAC 1200
TGGTCACCTG TTAAAAGCA AACATCTTAT TGGTTGCTAT GGGTTACTGC TTCTGGGCAA 1260
AATGTGTGCC TCATAGGGGG GTTAGTGTGT TGTGTACTGA ATTAATTGTA TTTATTTTCA 1320
TGTTACAATG AAGAGGATGT CTATGTTTAT TTCACTTTTA TTAATGTACA ATAAATGTTC 1380
TTGTTTCTTT AAAAAAAAAA AAAAATCGA G 1411

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ser	Arg	Thr	Arg	Lys	Val	Asp	Ser	Leu	Leu	Leu	Ala	Ile	Pro	1	5	10	15	
Gly	Leu	Ala	Leu	Leu	Leu	Pro	Asn	Ala	Tyr	Cys	Ala	Ser	Cys	Glu	20	25	30		
Pro	Val	Arg	Ile	Pro	Met	Cys	Lys	Ser	Met	Pro	Trp	Asn	Met	Thr	Lys	35	40	45	
Met	Pro	Asn	His	Leu	His	His	Ser	Thr	Gln	Ala	Asn	Ala	Ile	Leu	Ala	50	55	60	
Ile	Glu	Gln	Phe	Glu	Gly	Leu	Leu	Thr	Thr	Glu	Cys	Ser	Gln	Asp	Leu	65	70	75	80
Leu	Phe	Phe	Leu	Cys	Ala	Met	Tyr	Ala	Pro	Ile	Cys	Thr	Ile	Asp	Phe	85	90	95	

Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys Glu Arg Ala Arg
 100 105 110
 Ala Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His Thr Trp Pro Glu
 115 120 125
 Ser Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg Gly Val Cys Ile
 130 135 140
 Ser Pro Glu Ala Ile Val Thr Val Glu Gln Gly Thr Asp Ser Met Pro
 145 150 155 160
 Asp Phe Ser Met Asp Ser Asn Asn Gly Asn Cys Gly Ser Gly Arg Glu
 165 170 175
 His Cys Lys Cys Lys Pro Met Lys Ala Thr Gln Lys Thr Tyr Leu Lys
 180 185 190
 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Val
 195 200 205
 Lys Cys His Asp Ala Thr Ala Ile Val Glu Val Lys Glu Ile Leu Lys
 210 215 220
 Ser Ser Leu Val Asn Ile Pro Lys Asp Thr Val Thr Leu Tyr Thr Asn
 225 230 235 240
 Ser Gly Cys Leu Cys Pro Gln Leu Val Ala Asn Glu Glu Tyr Ile Ile
 245 250 255
 Met Gly Tyr Glu Asp Lys Glu Arg Thr Arg Leu Leu Leu Val Glu Gly
 260 265 270
 Ser Leu Ala Glu Lys Trp Arg Asp Arg Leu Ala Lys Lys Val Lys Arg
 275 280 285
 Trp Asp Gln Lys Leu Arg Arg Pro Arg Lys Ser Lys Asp Pro Val Ala
 290 295 300
 Pro Ile Pro Asn Lys Asn Ser Asn Ser Arg Gln Ala Arg Ser
 305 310 315

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1875 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCCTT TCACACAGGA CTCCTGGCAG AGGTGAATGG TTAGCCCTAT GGATTGTTGGTT 60
TGTTGATTTT GACACATGAT TGATTGCTTT CAGATAGGAT TGAAGGACTT GGATTTTAT 120
CTAATCTGCG ACTTTTAAAT TATCTGAGTA ATTGTTTCATT TTGTATTGGA TGGGACTAAA 180
GATAAACTTA ACTCCTTGCT TTTGACTTGC CCATAAACTA TAAGGTGGGG TGAGTTGTAG 240
TTGCTTTTAC ATGTGCCCAG ATTTTCCCTG TATTCCCTGT ATTCCCTCTA AAGTAAGCCT 300
ACACATACAG GTTGGGCAGA ATAACAATGT CTCGAACAAG GAAAGTGGAC TCATTACTGC 360
TACTGGCCAT ACCTGGACTG GCGCTTCTCT TATTACCCAA TGCTTACTGT GCTTCGTGTG 420
AGCCTGTGCG GATCCCCATG TGCAAATCTA TGCCATGGAA CATGACCAAG ATGCCCCAACC 480
ATCTCCACCA CAGCACTCAA GCCAATGCCA TCCTGGCAAT TGAACAGTTT GAAGGTTTGC 540
TGACCACTGA ATGTAGCCAG GACCTTTTGT TCTTTCTGTG TGCCATGTAT GCCCCCATTT 600
GTACCATCGA TTTCCAGCAT GAACCAATTA AGCCTTGCAA GTCCGTGTGC GAAAGGGCCA 660
GGGCCGGCTG TGAGCCCATT CTCATAAAGT ACCGGCACAC TTGGCCAGAG AGCCTGGCAT 720
GTGAAGAGCT GCCCGTATAT GACAGAGGAG TCTGCATCTC CCCAGAGGCT ATCGTCACAG 780
TGGAACAAGG AACAGATTCA ATGCCAGACT TCTCCATGGA TTCAAACAAT GGAAATTGCG 840
GAAGCGGCAG GGAGCACTGT AAATGCAAGC CCATGAAGGC AACCCAAAAG ACGTATCTCA 900
AGAATAATTA CAATTATGTA ATCAGAGCAA AAGTGAAAGA GGTGAAAGTG AAATGCCACG 960
ACGCAACAGC AATTGTGGAA GTAAAGGAGA TTCTCAAGTC TTCCCTAGTG AACATTCCTA 1020
AAGACACAGT GACACTGTAC ACCAACTCAG GCTGCTTGTG CCCCAGCTT GTTGCCAATG 1080
AGGAATACAT AATTATGGGC TATGAAGACA AAGAGCGTAC CAGGCTTCTA CTAGTGGAAG 1140
GATCCTTGGC CGAAAAATGG AGAGATCGTC TTGCTAAGAA AGTCAAGCGC TGGGATCAAA 1200
AGCTTCGACG TCCCAGGAAA AGCAAAGACC CCGTGGCTCC AATTCCTAAC AAAACAGCA 1260
ATTCCAGACA AGCGCGTAGT TAGACTAACG GAAAGGTGTA TGGAACTCT ATGGACTTTG 1320
AAACTAAGAT TTGCATTGTT GGAAGAGCAA AAAAGAAATT GCACTACAGC ACGTTATATT 1380
CTATTGTTTA CTACAAGAAG CTGGTTTAGT TGATTGTAGT TCTCCTTTCC TTCTTTTTTT 1440

TTATAACTAT ATTTGCACGT GTTCCCAGGC AATTGTTTTA TTCAACTTCC AGTGACAGAG 1500
 CAGTGACTGA ATGTCTCAGC CTAAAGAAGC TCAATTCATT TCTGATCAAC TAATGGTGAC 1560
 AAGTGTTTGA TACTTGGGGA AAGTGA ACTA ATTGCAATGG TAAATCAGAG AAAAGTTGAC 1620
 CAATGTTGCT TTTCCTGTAG ATGAACAAGT GAGAGATCAC ATTTAAATGA TGATCACTTT 1680
 CCATTTAATA CTTTCAGCAG TTTTAGTTAG ATGACATGTA GGATGCACCT AAATCTAAAT 1740
 ATTTTATCAT AAATGAAGAG CTGGTTTAGA CTGTATGGTC ACTGTTGGGA AGGTAAATGC 1800
 CTA CTTTGTC AATTCTGTTT TAAAAATTGC CTAAATAAAT ATTAAGTCCT AAATAAAAAA 1860
 AAAAAAAAAA AAAAA 1875

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 979 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Leu	Leu	Leu	Phe	Arg	Ala	Ile	Pro	Met	Leu	Leu	Leu	Gly	Leu	Met	1	5	10	15
Val	Leu	Gln	Thr	Asp	Cys	Glu	Ile	Ala	Gln	Tyr	Tyr	Ile	Asp	Glu	Glu	20	25	30	
Glu	Pro	Pro	Gly	Thr	Val	Ile	Ala	Val	Leu	Ser	Gln	His	Ser	Ile	Phe	35	40	45	
Asn	Thr	Thr	Asp	Ile	Pro	Ala	Thr	Asn	Phe	Arg	Leu	Met	Lys	Gln	Phe	50	55	60	
Asn	Asn	Ser	Leu	Ile	Gly	Val	Arg	Glu	Ser	Asp	Gly	Gln	Leu	Ser	Ile	65	70	75	80
Met	Glu	Arg	Ile	Asp	Arg	Glu	Gln	Ile	Cys	Arg	Gln	Ser	Leu	His	Cys	85	90	95	
Asn	Leu	Ala	Leu	Asp	Val	Val	Ser	Phe	Ser	Lys	Gly	His	Phe	Lys	Leu	100	105	110	

Leu	Asn	Val	Lys	Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	His	Ser	Pro	His
	115						120					125			
Phe	Pro	Ser	Glu	Ile	Met	His	Val	Glu	Val	Ser	Glu	Ser	Ser	Ser	Val
	130					135					140				
Gly	Thr	Arg	Ile	Pro	Leu	Glu	Ile	Ala	Ile	Asp	Glu	Asp	Val	Gly	Ser
145					150					155					160
Asn	Ser	Ile	Gln	Asn	Phe	Gln	Ile	Ser	Asn	Asn	Ser	His	Phe	Ser	Ile
				165					170					175	
Asp	Val	Leu	Thr	Arg	Ala	Asp	Gly	Val	Lys	Tyr	Ala	Asp	Leu	Val	Leu
			180					185					190		
Met	Arg	Glu	Leu	Asp	Arg	Glu	Ile	Gln	Pro	Thr	Tyr	Ile	Met	Glu	Leu
		195					200					205			
Leu	Ala	Met	Asp	Gly	Gly	Val	Pro	Ser	Leu	Ser	Gly	Thr	Ala	Val	Val
	210					215					220				
Asn	Ile	Arg	Val	Leu	Asp	Phe	Asn	Asp	Asn	Ser	Pro	Val	Phe	Glu	Arg
225					230					235					240
Ser	Thr	Ile	Ala	Val	Asp	Leu	Val	Glu	Asp	Ala	Pro	Leu	Gly	Tyr	Leu
				245					250					255	
Leu	Leu	Glu	Leu	His	Ala	Thr	Asp	Asp	Asp	Glu	Gly	Val	Asn	Gly	Glu
			260					265					270		
Ile	Val	Tyr	Gly	Phe	Ser	Thr	Leu	Ala	Ser	Gln	Glu	Val	Arg	Gln	Leu
		275					280					285			
Phe	Lys	Ile	Asn	Ser	Arg	Thr	Gly	Ser	Val	Thr	Leu	Glu	Gly	Gln	Val
	290					295					300				
Asp	Phe	Glu	Thr	Lys	Gln	Thr	Tyr	Glu	Phe	Glu	Val	Gln	Ala	Gln	Asp
305					310					315					320
Leu	Gly	Pro	Asn	Pro	Leu	Thr	Ala	Thr	Cys	Lys	Val	Thr	Val	His	Ile
				325					330					335	
Leu	Asp	Val	Asn	Asp	Asn	Thr	Pro	Ala	Ile	Thr	Ile	Thr	Pro	Leu	Thr
			340					345					350		
Thr	Val	Asn	Ala	Gly	Val	Ala	Tyr	Ile	Pro	Glu	Thr	Ala	Thr	Lys	Glu
		355					360					365			
Asn	Phe	Ile	Ala	Leu	Ile	Ser	Thr	Thr	Asp	Arg	Ala	Ser	Gly	Ser	Asn
	370					375					380				

Gly 385	Gln	Val	Arg	Cys	Thr 390	Leu	Tyr	Gly	His	Glu 395	His	Phe	Lys	Leu	Gln 400
Gln	Ala	Tyr	Glu	Asp 405	Ser	Tyr	Met	Ile	Val 410	Thr	Thr	Ser	Thr	Leu	Asp 415
Arg	Glu	Asn	Ile 420	Ala	Ala	Tyr	Ser	Leu	Thr 425	Val	Val	Ala	Glu	Asp	Leu 430
Gly	Phe	Pro 435	Ser	Leu	Lys	Thr	Lys 440	Lys	Tyr	Tyr	Thr	Val 445	Lys	Val	Ser
Asp	Glu 450	Asn	Asp	Asn	Ala	Pro 455	Val	Phe	Ser	Lys	Pro 460	Gln	Tyr	Glu	Ala
Ser 465	Ile	Leu	Glu	Asn	Asn 470	Ala	Pro	Gly	Ser	Tyr 475	Ile	Thr	Thr	Val	Ile 480
Ala	Arg	Asp	Ser	Asp 485	Ser	Asp	Gln	Asn	Gly 490	Lys	Val	Asn	Tyr	Arg	Leu 495
Val	Asp	Ala	Lys 500	Val	Met	Gly	Gln	Ser 505	Leu	Thr	Thr	Phe	Val 510	Ser	Leu
Asp	Ala	Asp 515	Ser	Gly	Val	Leu	Arg 520	Ala	Val	Arg	Ser	Leu 525	Asp	Tyr	Glu
Lys	Leu 530	Lys	Gln	Leu	Asp	Phe 535	Glu	Ile	Glu	Ala	Ala 540	Asp	Asn	Gly	Ile
Pro 545	Gln	Leu	Ser	Thr	Arg 550	Val	Gln	Leu	Asn	Leu 555	Arg	Ile	Val	Asp	Gln 560
Asn	Asp	Asn	Cys	Pro 565	Val	Ile	Thr	Asn	Pro 570	Leu	Leu	Asn	Asn	Gly 575	Ser
Gly	Glu	Val	Leu 580	Leu	Pro	Ile	Ser	Ala 585	Pro	Gln	Asn	Tyr	Leu 590	Val	Phe
Gln	Leu	Lys 595	Ala	Glu	Asp	Ser	Asp 600	Glu	Gly	His	Asn	Ser 605	Gln	Leu	Phe
Tyr	Thr 610	Ile	Leu	Arg	Asp	Pro 615	Ser	Arg	Leu	Phe	Ala 620	Ile	Asn	Lys	Glu
Ser 625	Gly	Glu	Val	Phe	Leu 630	Lys	Lys	Gln	Leu	Asn 635	Ser	Asp	His	Ser	Glu 640
Asp	Leu	Ser	Ile	Val 645	Val	Ala	Val	Tyr	Asp 650	Leu	Gly	Arg	Pro	Ser	Leu 655

Ser	Thr	Asn	Ala	Thr	Val	Lys	Phe	Ile	Leu	Thr	Asp	Ser	Phe	Pro	Ser
			660					665					670		
Asn	Val	Glu	Val	Val	Ile	Leu	Gln	Pro	Ser	Ala	Glu	Glu	Gln	His	Gln
		675					680					685			
Il	Asp	Met	Ser	Ile	Ile	Phe	Ile	Ala	Val	Leu	Ala	Gly	Gly	Cys	Ala
	690					695					700				
Leu	Leu	Leu	Leu	Ala	Ile	Phe	Phe	Val	Ala	Cys	Thr	Cys	Lys	Lys	Lys
705					710					715					720
Ala	Gly	Glu	Phe	Lys	Gln	Val	Pro	Glu	Gln	His	Gly	Thr	Cys	Asn	Glu
				725					730					735	
Glu	Arg	Leu	Leu	Ser	Thr	Pro	Ser	Pro	Gln	Ser	Val	Ser	Ser	Ser	Leu
			740					745					750		
Ser	Gln	Ser	Glu	Ser	Cys	Gln	Leu	Ser	Ile	Asn	Thr	Glu	Ser	Glu	Asn
		755					760					765			
Cys	Ser	Val	Ser	Ser	Asn	Gln	Glu	Gln	His	Gln	Gln	Thr	Gly	Ile	Lys
	770					775					780				
His	Ser	Ile	Ser	Val	Pro	Ser	Tyr	His	Thr	Ser	Gly	Trp	His	Leu	Asp
785					790					795					800
Asn	Cys	Ala	Met	Ser	Ile	Ser	Gly	His	Ser	His	Met	Gly	His	Ile	Ser
				805					810					815	
Thr	Lys	Asp	Ser	Gly	Lys	Gly	Asp	Ser	Asp	Phe	Asn	Asp	Ser	Asp	Ser
			820					825					830		
Asp	Thr	Ser	Gly	Glu	Ser	Gln	Lys	Lys	Ser	Ile	Glu	Gln	Pro	Met	Gln
		835					840					845			
Ala	Gln	Ala	Ser	Ala	Gln	Tyr	Thr	Asp	Glu	Ser	Ala	Gly	Phe	Arg	His
	850					855					860				
Ala	Asp	Asn	Tyr	Phe	Ser	His	Arg	Ile	Asn	Lys	Gly	Pro	Glu	Asn	Gly
865					870					875					880
Asn	Cys	Thr	Leu	Gln	Tyr	Glu	Lys	Gly	Tyr	Arg	Leu	Ser	Tyr	Ser	Val
				885					890					895	
Ala	Pro	Ala	His	Tyr	Asn	Thr	Tyr	His	Ala	Arg	Met	Pro	Asn	Leu	His
			900					905					910		
Ile	Pro	Asn	His	Thr	Leu	Arg	Asp	Pro	Tyr	Tyr	His	Ile	Asn	Asn	Pro
		915					920					925			

Val Ala Asn Arg Met His Ala Glu Tyr Glu Arg Asp Leu Val Asn Arg
 930 935 940

Ser Ala Thr Leu Ser Pro Gln Arg Ser Ser Ser Arg Tyr Gln Glu Phe
 945 950 955 960

Asn Tyr Ser Pro Gln Ile Ser Arg Gln Leu His Pro Ser Glu Ile Ala
 965 970 975

Thr Thr Phe

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTC	CCCAG	AGATGA	ACTC	CTTGAG	ATTG	TTTTAA	ATGA	CTGCAG	GTCT	GGAAGG	ATTC	60
ACATTG	CCAC	ACTGTT	TCTA	GGCATG	AAAA	AACTGC	AAAGT	TTCAAC	TTTG	TTTTTG	GTGC	120
AACTTT	GATT	CTTCAAG	ATG	CTGCTT	CTCT	TCAGAG	CCAT	TCCAAT	GCTG	CTGTTG	GGGAC	180
TGATGG	TTTT	ACAAAC	AGAC	TGTGAA	ATTG	CCCAGT	ACTA	CATAGAT	GAA	GAAGAACC	CCCC	240
CTGGCA	CTGT	AATTGC	AGTG	TTGTCAC	AAC	ACTCCAT	ATT	TAACACT	ACA	GATATAC	CTG	300
CAACCA	ATTT	CCGTCT	AATG	AAGCAAT	TTA	ATAATT	CCCT	TATCGG	AGTC	CGTGAG	AGTG	360
ATGGGC	CAGCT	GAGCAT	CATG	GAGAGG	ATTG	ACCGGG	AGCA	AATCTG	CAGG	CAGTCC	CTTC	420
ACTGCA	ACCT	GGCTTT	GGAT	GTGGTC	AGCT	TTTCCA	AAGG	ACACTT	CAAG	CTTCTG	AACG	480
TGAAAG	TGGA	GGTGAG	AGAC	ATTAAT	GACC	ATAGCC	CCTCA	CTTTCC	CAGT	GAAATA	ATGC	540
ATGTGG	GAGGT	GTCTGA	AAGT	TCCTCT	GTGG	GCACCAG	GAT	TCCTTT	AGAA	ATTGCA	ATAG	600
ATGAAG	ATGT	TGGGTCC	AAC	TCCATCC	AGA	ACTTTC	AGAT	CTCAA	ATAAT	AGCCACT	TCA	660
GCATTG	ATGT	GCTAAC	CAGA	GCAGAT	G G G G	TGAAAT	ATGC	AGATT	TAGTC	TTAATG	AGAG	720
AACTGG	ACAG	GGAAAT	CCAG	CCAACAT	ACA	TAATGG	AGCT	ACTAGC	AAATG	GATGGG	GGTG	780

TACCATCACT	ATCTGGTACT	GCAGTGGTTA	ACATCCGAGT	CCTGGACTTT	AATGATAACA	840
GCCCAGTGTT	TGAGAGAAGC	ACCATTGCTG	TGGACCTAGT	AGAGGATGCT	CCTCTGGGAT	900
ACCTTTTGTT	GGAGTTACAT	GCTACTGACG	ATGATGAAGG	AGTGAATGGA	GAAATTGTTT	960
ATGGATTCAG	CACTTTGGCA	TCTCAAGAGG	TACGTCAGCT	ATTTAAAATT	AACTCCAGAA	1020
CTGGCAGTGT	TACTCTTGAA	GGCCAAGTTG	ATTTTGAGAC	CAAGCAGACT	TACGAATTTG	1080
AGGTACAAGC	CCAAGATTTG	GGCCCCAACC	CACTGACTGC	TACTTGTAAG	GTAAGTGTTC	1140
ATATACTTGA	TGTAAATGAT	AATACCCAG	CCATCACTAT	TACCCCTCTG	ACTACTGTAA	1200
ATGCAGGAGT	TGCCTATATT	CCAGAAACAG	CCACAAAGGA	GAAGTTTATA	GCTCTGATCA	1260
GCACTACTGA	CAGAGCCTCT	GGATCTAATG	GACAAGTTCG	CTGTACTCTT	TATGGACATG	1320
AGCACTTTAA	ACTACAGCAA	GCTTATGAGG	ACAGTTACAT	GATAGTTACC	ACCTCTACTT	1380
TAGACAGGGA	AAACATAGCA	GCGTACTCTT	TGACAGTAGT	TGCAGAAGAC	CTTGGCTTCC	1440
CCTCATTGAA	GACCAAAAAG	TACTACACAG	TCAAGGTTAG	TGATGAGAAT	GACAATGCAC	1500
CTGTATTTTC	TAAACCCAG	TATGAAGCTT	CTATTCTGGA	AAATAATGCT	CCAGGCTCTT	1560
ATATACTAC	AGTGATAGCC	AGAGACTCTG	ATAGTGATCA	AAATGGCAAA	GTAAATTACA	1620
GAAGTTGTGA	TGCAAAAGTG	ATGGGCCAGT	CACTAACAAC	ATTTGTTTCT	CTTGATGCGG	1680
ACTCTGGAGT	ATTGAGAGCT	GTTAGGTCTT	TAGACTATGA	AAAAGTTAAA	CAAGTGGATT	1740
TTGAAATTGA	AGCTGCAGAC	AATGGGATCC	CTCAACTCTC	CACTCGCGTT	CAAGTAAATC	1800
TCAGAATAGT	TGATCAAAAT	GATAATTGCC	CTGTGATAAC	TAATCCTCTT	CTTAATAATG	1860
GCTCGGGTGA	AGTTCTGCTT	CCCATCAGCG	CTCCTCAAAA	CTATTTAGTT	TTCCAGCTCA	1920
AAGCCGAGGA	TTCAGATGAA	GGGCACAACT	CCCAGCTGTT	CTATACCATA	CTGAGAGATC	1980
CAAGCAGATT	GTTTGCCATT	AACAAAGAAA	GTGGTGAAGT	GTTTCTGAAA	AAACAATTAA	2040
ACTCTGACCA	TTCAGAGGAC	TTGAGCATAG	TAGTTGCAGT	GTATGACTTG	GGAAGACCTT	2100
CATTATCCAC	CAATGCTACA	GTTAAATTCA	TCCTCACCGA	CTCTTTTCCT	TCTAACGTTG	2160
AAGTCGTTAT	TTTGCAACCA	TCTGCAGAAG	AGCAGCACCA	GATCGATATG	TCCATTATAT	2220
TCATTGCAGT	GCTGGCTGGT	GGTTGTGCTT	TGCTACTTTT	GGCCATCTTT	TTTGTGGCCT	2280
GTAAGTTGTAA	AAAGAAAGCT	GGTGAATTTA	AGCAGGTACC	TGAACAACAT	GGAACATGCA	2340

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Val Cys Cys Gly Pro Gly Arg Met Leu Leu Gly Trp Ala Gly Leu
1 5 10 15
Leu Val Leu Ala Ala Leu Cys Leu Leu Gln Val Pro Gly Ala Gln Ala
20 25 30
Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
35 40 45
Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
50 55 60
Ala Ile Leu Ala Met Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
65 70 75 80
Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
85 90 95
Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
100 105 110
Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
115 120 125
Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu Pro Val Tyr Asp Arg
130 135 140
Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
145 150 155 160
Phe Pro Met Asp Ser Ser Thr Gly His Cys Arg Gly Ala Ser Ser Glu
165 170 175
Arg Cys Lys Cys Lys Pro Val Arg Ala Thr Gln Lys Thr Tyr Phe Arg
180 185 190
Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Met
195 200 205
Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
210 215 220
Ala Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Thr
225 230 235 240

Ser Gly Cys Leu Cys Pro Pro Leu Thr Val Asn Glu Glu Tyr Val Ile
245 250 255

Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
260 265 270

Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
275 280 285

Trp Asp Met Lys Leu Arg His Leu Gly Leu Gly Lys Thr Asp Ala Ser
290 295 300

Asp Ser Thr Gln Asn Gln Lys Ser Gly Arg Asn Ser Asn Pro Arg Pro
305 310 315 320

Ala Arg Ser

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGCCTGGGA CCATGGTCTG CTGCGGCCCG GGACGGATGC TGCTAGGATG GGCCGGGTTG	60
CTAGTCCTGG CTGCTCTCTG CCTGCTCCAG GTGCCCCGAG CTCAGGCTGC AGCCTGTGAG	120
CCTGTCCGCA TCCCGCTGTG CAAGTCCCTT CCCTGGAACA TGACCAAGAT GCCCAACCAC	180
CTGCACCACA GCACCCAGGC TAACGCCATC CTGGCCATGG AACAGTTCGA AGGGCTGCTG	240
GGCACCCACT GCAGCCCGGA TCTTCTCTTC TTCCTCTGTG CAATGTACGC ACCCATTTGC	300
ACCATCGACT TCCAGCACGA GCCCATCAAG CCCTGCAAGT CTGTGTGTGA GCGCGCCCGA	360
CAGGGCTGCG AGCCCATTTCT CATCAAGTAC CGCCACTCGT GGCCGGAAAG CTTGGCCTGC	420
GACGAGCTGC CGGTGTACGA CCGCGGCGTG TGCATCTCTC CTGAGGCCAT CGTCACCGCG	480
GACGGAGCGG ATTTTCCTAT GGATTCAAGT ACTGGACACT GCAGAGGGGC AAGCAGCGAA	540
CGTTGCAAAT GTAAGCCTGT CAGAGCTACA CAGAAGACCT ATTTCCGGAA CAATTACAAC	600

TATGTCATCC	GGGCTAAAGT	TAAAGAGGTA	AAGATGAAAT	GTCATGATGT	GACCGCCGTT	660
GTGGAAGTGA	AGGAAATTCT	AAAGGCATCA	CTGGTAAACA	TTCCAAGGGA	CACCGTCAAT	720
CTTTATACCA	CCTCTGGCTG	CCTCTGTCCT	CCACTTACTG	TCAATGAGGA	ATATGTCATC	780
ATGGGCTATG	AAGACGAGGA	ACGTTCCAGG	TTACTCTTGG	TAGAAGGCTC	TATAGCTGAG	840
AAGTGGAAGG	ATCGGCTTGG	TAAGAAAGTC	AAGCGCTGGG	ATATGAAACT	CCGACACCTT	900
GGACTGGGTA	AAACTGATGC	TAGCGATTCC	ACTCAGAATC	AGAAGTCTGG	CAGGAACTCT	960
AATCCCCGGC	CAGCACGCAG	CTAAATCCTG	AAATGTAAAA	GGCCACACCC	ACGGACTCCC	1020
TTCTAAGACT	GGCGCTGGTG	GACTAACAAA	GGAAAACCGC	ACAGTTGTGC	TCGTGACCGA	1080
TTGTTTACCG	CAGACACCGC	GTGGCTACCG	AAGTTACTTC	CGGTCCCCTT	TCTCCTGCTT	1140
CTTAATGGCG	TGGGGTTAGA	TCCTTTAATA	TGTTATATAT	TCTGTTTCAT	CAATCACGTG	1200
GGGACTGTTC	TTTTGCAACC	AGAATAGTAA	ATTAAATATG	TTGATGCTAA	GGTTTCTGTA	1260
CTGGACTCCC	TGGGTTTAAT	TTGGTGTTCT	GTACCCTGAT	TGAGAATGCA	ATGTTTCATG	1320
TAAAGAGAGA	ATCCTGGTCA	TATCTCAAGA	ACTAGATATT	GCTGTAAGAC	AGCCTCTGCT	1380
GCTGCGCTTA	TAGTCTTG TG	TTTGTATGCC	TTTGTCCATT	TCCCTCATGC	TGTGAAAGTT	1440
ATACATGTTT	ATAAAGGTAG	AACGGCATT T	TGAAATCAGA	CACTGCACAA	GCAGAGTAGC	1500
CCAACACCAG	GAAGCATTTA	TGAGGAAACG	CCACACAGCA	TGACTTATTT	TCAAGATTGG	1560
CAGGCAGCAA	AATAAATAGT	GTTGGGAGCC	AAGAAAAGAA	TATTTTGCCT	GGTTAAGGGG	1620
CACACTGGAA	TCAGTAGCCC	TTGAGCCATT	AACAGCAGTG	TTCTTCTGGC	AAGTTTTTGA	1680
TTTGTTCATA	AATGTATTCA	CGAGCATTAG	AGATGAACTT	ATAACTAGAC	ATCTGTTGTT	1740
ATCTCTATAG	CTCTGCTTCC	TTCTAAATCA	AACCCATTGT	TGGATGCTCC	CTCTCCATTC	1800
ATAAATAAAT	TTGGCTTGCT	GTATTGGCCA	GGAAAAGAAA	GTATTAAAGT	ATGCATGCAT	1860
GTGCACCAGG	GTGTTATTTA	ACAGAGGTAT	GTAAC TCTAT	AAAAGACTAT	AATTTACAGG	1920
ACACGGAAAT	GTGCACATTT	GTTTACTTTT	TTTCTTCCTT	TTGCTTTGGG	CTTGTGATTT	1980
TGGTTTTTGG	TGTGTTTATG	TCTGTATTTT	GGGGGGTGGG	TAGGTTTAAG	CCATTGCACA	2040
TTCAAGTTGA	ACTAGATTAG	AGTAGACTAG	GCTCATTGGC	CTAGACATTA	TGATTTGAAT	2100

TTGTGTTGTT TAATGCTCCA TCAAGATGTC TAATAAAAGG AATATGGTTG TCAACAGAGA 2160
CGACAACAAC AACAAA 2176

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Val	Cys	Gly	Ser	Pro	Gly	Gly	Met	Leu	Leu	Leu	Arg	Ala	Gly	Leu	1	5	10	15
Leu	Ala	Leu	Ala	Ala	Leu	Cys	Leu	Leu	Arg	Val	Pro	Gly	Ala	Arg	Ala	20	25	30	
Ala	Ala	Cys	Glu	Pro	Val	Arg	Ile	Pro	Leu	Cys	Lys	Ser	Leu	Pro	Trp	35	40	45	
Asn	Met	Thr	Lys	Met	Pro	Asn	His	Leu	His	His	Ser	Thr	Gln	Ala	Asn	50	55	60	
Ala	Ile	Leu	Ala	Ile	Glu	Gln	Phe	Glu	Gly	Leu	Leu	Gly	Thr	His	Cys	65	70	75	80
Ser	Pro	Asp	Leu	Leu	Phe	Phe	Leu	Cys	Ala	Met	Tyr	Ala	Pro	Ile	Cys	85	90	95	
Thr	Ile	Asp	Phe	Gln	His	Glu	Pro	Ile	Lys	Pro	Cys	Lys	Ser	Val	Cys	100	105	110	
Glu	Arg	Ala	Arg	Gln	Gly	Cys	Glu	Pro	Ile	Leu	Ile	Lys	Tyr	Arg	His	115	120	125	
Ser	Trp	Pro	Glu	Asn	Leu	Ala	Cys	Glu	Glu	Leu	Pro	Val	Tyr	Asp	Arg	130	135	140	
Gly	Val	Cys	Ile	Ser	Pro	Glu	Ala	Ile	Val	Thr	Ala	Asp	Gly	Ala	Asp	145	150	155	160
Phe	Pro	Met	Asp	Ser	Ser	Asn	Gly	Asn	Cys	Arg	Gly	Ala	Ser	Ser	Glu	165	170	175	

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Arg	Cys	Lys	Cys	Lys	Pro	Ile	Arg	Ala	Thr	Gln	Lys	Thr	Tyr	Phe	Arg
			180					185					190		
Asn	Asn	Tyr	Asn	Tyr	Val	Ile	Arg	Ala	Lys	Val	Lys	Glu	Ile	Lys	Thr
		195					200					205			
Lys	Cys	His	Asp	Val	Thr	Ala	Val	Val	Glu	Val	Lys	Glu	Ile	Leu	Lys
	210					215					220				
Ser	Ser	Leu	Val	Asn	Ile	Pro	Arg	Asp	Thr	Val	Asn	Leu	Tyr	Thr	Ser
225					230					235					240
Ser	Gly	Cys	Leu	Cys	Pro	Pro	Leu	Asn	Val	Asn	Glu	Glu	Tyr	Ile	Ile
				245					250					255	
Met	Gly	Tyr	Glu	Asp	Glu	Glu	Arg	Ser	Arg	Leu	Leu	Leu	Val	Glu	Gly
			260					265					270		
Ser	Ile	Ala	Glu	Lys	Trp	Lys	Asp	Arg	Leu	Gly	Lys	Lys	Val	Lys	Arg
		275					280					285			
Trp	Asp	Met	Lys	Leu	Arg	His	Leu	Gly	Leu	Ser	Lys	Ser	Asp	Ser	Ser
	290					295					300				
Asn	Ser	Asp	Ser	Thr	Gln	Ser	Gln	Lys	Ser	Gly	Arg	Asn	Ser	Asn	Pro
305					310					315					320
Arg	Gln	Ala	Arg	Asn											
				325											

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1893 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGCGGAGCGG GCCTTTTGGC GTCCACTGCG CGGCTGCACC CTGCCCCATC TGCCGGGATC	60
ATGGTCTGCG GCAGCCCGGG AGGGATGCTG CTGCTGCGGG CCGGGCTGCT TGCCCTGGCT	120
GCTCTCTGCC TGCTCCGGGT GCCCGGGGCT CGGGCTGCAG CCTGTGAGCC CGTCCGCATC	180
CCCCTGTGCA AGTCCCTGCC CTGGAACATG ACTAAGATGC CCAACCACCT GCACCACAGC	240

ACTCAGGCCA	ACGCCATCCT	GGCCATCGAG	CAGTTCGAAG	GTCTGCTGGG	CACCCACTGC	300
AGCCCCGATC	TGCTCTTCTT	CCTCTGTGCC	ATGTACGCGC	CCATCTGCAC	CATTGACTTC	360
CAGCACGAGC	CCATCAAGCC	CTGTAAGTCT	GTGTGCGAGC	GGGCCCCGCA	GGGCTGTGAG	420
CCCATACTCA	TCAAGTACCG	CCACTCGTGG	CCGGAGAACC	TGGCCTGCGA	GGAGCTGCCA	480
GTGTACGACA	GGGGCGTGTG	CATCTCTCCC	GAGGCCATCG	TTACTGCGGA	CGGAGCTGAT	540
TTTCCTATGG	ATTCTAGTAA	CGGAAACTGT	AGAGGGGCAA	GCAGTGAACG	CTGTAAATGT	600
AAGCCTATTA	GAGCTACACA	GAAGACCTAT	TTCCGGAACA	ATTACAACATA	TGTCATTTCGG	660
GCTAAAGTTA	AAGAGATAAA	GACTAAGTGC	CATGATGTGA	CTGCAGTAGT	GGAGGTGAAG	720
GAGATTCTAA	AGTCCTCTCT	GGTAAACATT	CCACGGGACA	CTGTCAACCT	CTATACCAGC	780
TCTGGCTGCC	TCTGCCCTCC	ACTTAATGTT	AATGAGGAAT	ATATCATCAT	GGGCTATGAA	840
GATGAGGAAC	GTTCCAGATT	ACTCTTGGTG	GAAGGCTCTA	TAGCTGAGAA	GTGGAAGGAT	900
CGACTCGGTA	AAAAAGTTAA	GCGCTGGGAT	ATGAAGCTTC	GTCATCTTGG	ACTCAGTAAA	960
AGTGATTCTA	GCAATAGTGA	TTCCACTCAG	AGTCAGAAGT	CTGGCAGGAA	CTCGAACCCC	1020
CGGCAAGCAC	GCAACTAAAT	CCCGAAATAC	AAAAAGTAAC	ACAGTGGACT	TCCTATTAAG	1080
ACTTACTTGC	ATTGCTGGAC	TAGCAAAGGA	AAATTGCACT	ATTGCACATC	ATATTCTATT	1140
GTTTACTATA	AAAATCATGT	GATAACTGAT	TATTACTTCT	GTTTCTCTTT	TGGTTTCTGC	1200
TTCTCTCTTC	TCTCAACCCC	TTTGTAATGG	TTTGGGGGCA	GACTCTTAAG	TATATTGTGA	1260
GTTTTCTATT	TCACTAATCA	TGAGAAAAAC	TGTTCTTTTG	CAATAATAAT	AAATTAAACA	1320
TGCTGTTACC	AGAGCCTCTT	TGCTGAGTCT	CCAGATGTTA	ATTTACTTTC	TGCACCCCAA	1380
TTGGGAATGC	AATATTGGAT	GAAAAGAGAG	GTTTCTGGTA	TTCACAGAAA	GCTAGATATG	1440
CCTTAAAACA	TACTCTGCCG	ATCTAATTAC	AGCCTTATTT	TTGTATGCCT	TTTGGGCATT	1500
CTCCTCATGC	TTAGAAAGTT	CCAAATGTTT	ATAAAGGTAA	AATGGCAGTT	TGAAGTCAAA	1560
TGTCACATAG	GCAAAGCAAT	CAAGCACCAG	GAAGTGTTTA	TGAGGAAACA	ACACCCAAGA	1620
TGAATTATTT	TTGAGACTGT	CAGGAAGTAA	AATAAATAGG	AGCTTAAGAA	AGAACATTTT	1680
GCCTGATTGA	GAAGCACAAC	TGAAACCAGT	AGCCGCTGGG	GTGTTAATGG	TAGCATTCTT	1740
CTTTTGCAA	TACATTTGAT	TTGTTTCATGA	ATATATTAAT	CAGCATTAGA	GAAATGAATT	1800

ATAACTAGAC ATCTGCTGTT ATCACCATAG TTTTGTTTAA TTTGCTTCCT TTAAATAAA 1860

CCCATTGGTG AAATCAAAA AAAAAAAAAA AAA 1893

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